

REMARKS

By this amendment, the claims have been amended so as to more clearly define the subject matter of the present invention, and in particular, these amendments include the deletion of the term "identity" that has been the subject of the previous objections by the Examiner. As a result, the claims as amended now overcome all prior rejections and are in condition for allowance for the reasons as stated below.

In the Official Action, Claims 54-78 were rejected under 35 U.S.C. § 112, first paragraph, on the basis of the Examiner's argument that the phrase "maximal amino acid identity alignment . . ." was not disclosed in the specification because the specification did not "establish the relationship between homology and identity." Although Applicants contest this position¹, the Examiner's rejection has now become moot by virtue of the amendment to the present claims whereby the term "identity" has been eliminated from the claims. As presently amended, the claims now incorporate the use of the term "maximal amino acid alignment versus the total number of positions while introducing vacant positions artificially" which is set forth at page 11 of the specification, and which will allow one of ordinary skill in this art to make and use the present invention.

¹In fact, at page 11 of the specification, the degree of homology is clearly established by reckoning up all the positions where the amino acids of the two sequences under consideration are identical, relative to the number of positions, and thus relationship between homology and identity is clearly defined. Moreover, illustration of such a definition is provided in Figures 1-4.

In the Official Action, the Examiner rejected Claims 54-78 under 35 U.S.C. § 112, second paragraph, as being indefinite in that the claims referred to SEQ ID NOS 1 and 3 which were directed to DNA sequences. This rejection has been overcome in that the claims now properly refer to the amino acid sequences of SEQ ID NOS 2 and 4 which show the amino acid sequences originally disclosed in SEQ ID NOS 1 and 3, respectively.

In addition, the Examiner rejected Claims 54-78 by virtue of the use of the phrase "maximal amino acid identity alignment . . ." which the Examiner argued would not be able to adequately define "identity" without "precise algorithms with parameters." This rejection has now become moot by the present amendments to the claims which delete the term "identity" from the claims and make clear the precise steps necessary for one skilled in the art to make and use the claimed invention. Even further, the Examiner in the Official Action argued that the prior claims were not definite because in a hypothetical alignment, the amino acids could be compared in four ways, as follows:

(a) acgtac 4/6 = 67%

(c) acgtac 2/6 = 33%

(b) ac—ac 4/4 = 100%

(d) acac 2/4 = 50%

However, the Examiner's hypothetical, to the extent it is still applied to the claims as amended, is incorrect in that Applicants' specification and claims clearly teach that the alignment shall be maximal and that vacant positions shall be artificially introduced and taken into account for maximal alignment. Accordingly, the only possible approach for alignment is the one indicated as hypothetical "(a)" above, and all others are not applicable because they do not provide for maximal alignment.

Additionally, the reference cited by the Examiner (George et al., page 130) has been considered by Applicants, and Applicants submit that the present application is in compliance with the specified requirements. As set forth therein, it is stated that "the most important decision that must be made in sequence comparison is the choice of scoring rules. In any sequence comparison application, whether it be database searching pattern recognition, or sequence alignment, the best solution is selected from all other possible solutions raised on a predefined set of scoring rules: this generally involves assigning a score to each possible alignment or subalignment and selecting those with the 'best' scores. The results of the analysis are entirely dependent on the choice of scoring rules." In compliance with this passage, the present specification and claims provide for a scoring rule as it is taught that the alignment shall be maximal.

It is thus submitted that the application as amended is in full compliance with Section 112, and that the Examiner's rejection under this provision should be withdrawn.

In the Official Action, the Examiner rejected the claims under 35 U.S.C. § 102(b) on the basis of the Legrain et al. and Quentin-Millet references, arguing that Applicants' use of the term "obtained" in the claims encompassed "variants and derivatives because the claims encompass Tbp2 receptor [sic] which are 'obtained' from the amino acid identity alignment without algorithms or parameters to obtain a precise alignment or identity." In light of the amendments to the claims, the Examiner's rejection has become moot because the claims have been amended to delete reference to "identity", and these claims are now clearly defined to exclude the receptors of the prior art which are not obtained by total or partial deletion as is the case in the present claims.

Moreover, the term "obtained from" as used herein cannot be construed to encompass "variants and derivatives", i.e., changing one amino acid for another, as argued by the Examiner. To the contrary, the claims now make it clear that the sequence of the claimed polypeptide is one that is obtained by deletion, i.e., by total or partial deletion as set forth in the claim language. Since it is clear that polypeptide sequences obtained by total or partial deletion are not disclosed or suggested in the prior art references cited by the Examiner, nor does the Examiner so argue, the claims as presently amended are clearly not anticipated or made obvious by the cited Legrain and Quentin-Millet references, either singly or in combination.

Accordingly, Applicants submit that the Examiner's rejections under 35 U.S.C. § 102(b), insofar as applied to the claims as amended, are respectfully traversed and should be withdrawn.

In light of the foregoing amendment and arguments, Applicants thus submit that the present amendment overcomes the prior rejections by the Examiner and places the application in condition for allowance, and such action is earnestly solicited.

Respectfully submitted,


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